RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/042,583*

INPUT SET: S24576.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

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 1                               SEQUENCE LISTING
 2
 3    (1)    General Information:
 4
 5         (i) APPLICANT: Ni, Jian
 6                        Gentz, Reiner
 7                        Yu, Guo-Liang
 8                        Su, Jeffrey
 9                        Rosen, Craig A.
10
11       (ii) TITLE OF INVENTION: Death Domain Containing Receptor 5
12
13      (iii) NUMBER OF SEQUENCES: 12
14
15       (iv) CORRESPONDENCE ADDRESS:
16            (A) ADDRESSEE: Human Genome Sciences, Inc.
17            (B) STREET: 9410 Key West Avenue
18            (C) CITY: Rockville
19            (D) STATE: MD
20            (E) COUNTRY: US
21            (F) ZIP: 20850
22
23        (v) COMPUTER READABLE FORM:
24            (A) MEDIUM TYPE: Floppy disk
25            (B) COMPUTER: IBM PC compatible
26            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28
29       (vi) CURRENT APPLICATION DATA:
30            (A) APPLICATION NUMBER: US herewith
31            (B) FILING DATE:
32            (C) CLASSIFICATION:
33
34      (vii) PRIOR APPLICATION DATA:
35            (A) APPLICATION NUMBER: US 60/054,021
36            (B) FILING DATE: 29-JUL-1997
37
38      (vii) PRIOR APPLICATION DATA:
39            (A) APPLICATION NUMBER: US 60/040,846
40            (B) FILING DATE: 17-MAR-1997
41
42     (viii) ATTORNEY/AGENT INFORMATION:
43            (A) NAME: Hoover, Kenley
44            (B) REGISTRATION NUMBER: 40,302
45            (C) REFERENCE/DOCKET NUMBER: PF366
46
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PATENT APPLICATION   *US/09/042,583*

INPUT SET: S24576.raw

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47          (ix) TELECOMMUNICATION INFORMATION:
48                (A)  TELEPHONE: 3013098504
49                (B)  TELEFAX: 3013098439
50
51
52   (2) INFORMATION FOR SEQ ID NO:1:
53
54          (i)  SEQUENCE CHARACTERISTICS:
55                (A)  LENGTH: 1600 base pairs
56                (B)  TYPE: nucleic acid
57                (C)  STRANDEDNESS: single
58                (D)  TOPOLOGY: linear
59
60          (ii) MOLECULE TYPE: DNA (genomic)
61
62
63          (ix) FEATURE:
64                (A)  NAME/KEY: sig_peptide
65                (B)  LOCATION: 130..283
66
67          (ix) FEATURE:
68                (A)  NAME/KEY: CDS
69                (B)  LOCATION: 130..1362
70
71          (ix) FEATURE:
72                (A)  NAME/KEY: mat_peptide
73                (B)  LOCATION: 284..1362
74
75
76          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
77
78   CACGCGTCCG CGGGCGCGGC CGGAGAACCC CGCAATCTTT GCGCCCACAA AATACACCGA          60
79
80   CGATGCCCGA TCTACTTTAA GGGCTGAAAC CCACGGGCCT GAGAGACTAT AAGAGCGTTC         120
81
82   CCTACCGCC ATG GAA CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG             168
83             Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly
84             -51 -50                 -45                 -40
85
86   GCC CGG AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC AGG          216
87   Ala Arg Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg
88             -35                 -30                 -25
89
90   CCT GGG CCC CGG GTC CCC AAG ACC CTT GTG CTC GTT GTC GCC GCG GTC          264
91   Pro Gly Pro Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val
92             -20                 -15                 -10
93
94   CTG CTG TTG GTC TCA GCT GAG TCT GCT CTG ATC ACC CAA CAA GAC CTA          312
95   Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu
96             -5                  1                 5                   10
97
98   GCT CCC CAG CAG AGA GCG GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA          360
99   Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser
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PATENT APPLICATION   *US/09/042,583*

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100                    15                      20                      25
101
102  GAG GGA TTG TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT        408
103  Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp
104              30                      35                      40
105
106  TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC TGG AAT GAC        456
107  Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp
108              45                      50                      55
109
110  CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT GAT TCA GGT GAA GTG GAG        504
111  Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu
112              60                      65                      70
113
114  CTA AGT CCC TGC ACC ACG ACC AGA AAC ACA GTG TGT CAG TGC GAA GAA        552
115  Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu
116   75                      80                      85                  90
117
118  GGC ACC TTC CGG GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC        600
119  Gly Thr Phe Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg
120              95                      100                     105
121
122  ACA GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA CCC TGG        648
123  Thr Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp
124              110                     115                     120
125
126  AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC ATC ATC ATA GGA GTC        696
127  Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val
128              125                     130                     135
129
130  ACA GTT GCA GCC GTA GTC TTG ATT GTG GCT GTG TTT GTT TGC AAG TCT        744
131  Thr Val Ala Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser
132              140                     145                     150
133
134  TTA CTG TGG AAG AAA GTC CTT CCT TAC CTG AAA GGC ATC TGC TCA GGT        792
135  Leu Leu Trp Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly
136   155                     160                     165                 170
137
138  GGT GGT GGG GAC CCT GAG CGT GTG GAC AGA AGC TCA CAA CGA CCT GGG        840
139  Gly Gly Gly Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly
140              175                     180                     185
141
142  GCT GAG GAC AAT GTC CTC AAT GAG ATC GTG AGT ATC TTG CAG CCC ACC        888
143  Ala Glu Asp Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr
144              190                     195                     200
145
146  CAG GTC CCT GAG CAG GAA ATG GAA GTC CAG GAG CCA GCA GAG CCA ACA        936
147  Gln Val Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr
148              205                     210                     215
149
150  GGT GTC AAC ATG TTG TCC CCC GGG GAG TCA GAG CAT CTG CTG GAA CCG        984
151  Gly Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro
152              220                     225                     230
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153
154    GCA GAA GCT GAA AGG TCT CAG AGG AGG AGG CTG CTG GTT CCA GCA AAT     1032
155    Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn
156    235             240             245             250
157
158    GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT GAC TTT GCA     1080
159    Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala
160                    255             260             265
161
162    GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG CTC ATG AGG AAG TTG GGC     1128
163    Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly
164                    270             275             280
165
166    CTC ATG GAC AAT GAG ATA AAG GTG GCT AAA GCT GAG GCA GCG GGC CAC     1176
167    Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His
168            285             290             295
169
170    AGG GAC ACC TTG TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG     1224
171    Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly
172        300             305             310
173
174    CGA GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG CTG GGA     1272
175    Arg Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly
176    315             320             325             330
177
178    GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC TTG TTG AGC TCT GGA     1320
179    Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly
180                    335             340             345
181
182    AAG TTC ATG TAT CTA GAA GGT AAT GCA GAC TCT GCC ATG TCC             1362
183    Lys Phe Met Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
184                    350             355             360
185
186    TAAGTGTGAT TCTCTTCAGG AAGTGAGACC TTCCCTGGTT TACCTTTTTT CTGGAAAAAG   1422
187
188    CCCAACTGGA CTCCAGTCAG TAGGAAAGTG CCACAATTGT CACATGACCG GTACTGGAAG   1482
189
190    AAACTCTCCC ATCCAACATC ACCCAGTGGA TGGAACATCC TGTAACTTTT CACTGCACTT   1542
191
192    GGCATTATTT TTATAAGCTG AATGTGATAA TAAGGACACT ATGGAAAAAA AAAAAAAA     1600
193
194
195    (2) INFORMATION FOR SEQ ID NO:2:
196
197            (i) SEQUENCE CHARACTERISTICS:
198                (A) LENGTH: 411 amino acids
199                (B) TYPE: amino acid
200                (D) TOPOLOGY: linear
201
202            (ii) MOLECULE TYPE: protein
203
204            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
205
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206   Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
207   -51 -50                  -45              -40
208

209   Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro
210   -35              -30              -25              -20
211

212   Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
213               -15              -10              -5
214

215   Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
216               1               5               10
217

218   Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
219       15              20              25
220

221   Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
222   30              35              40              45
223

224   Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
225               50              55              60
226

227   Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
228           65              70              75
229

230   Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
231       80              85              90
232

233   Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
234       95              100             105
235

236   Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
237   110             115             120             125
238

239   Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala
240               130             135             140
241

242   Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
243           145             150             155
244

245   Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly
246           160             165             170
247

248   Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
249       175             180             185
250

251   Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
252   190             195             200             205
253

254   Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
255               210             215             220
256

257   Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
258               225             230             235
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/042,583*

INPUT SET: S24576.raw

Line	Error	Original Text
30	Wrong application Serial Number	(A) APPLICATION NUMBER: US herewith